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1638

TECH CENTER 1600/2900



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RAW SEQUENCE LISTING

DATE: 08/01/2002

PATENT APPLICATION: US/09/786,960

TIME: 11:13:50

Input Set : A:\10015.app

Output Set: N:\CRF3\08012002\I786960.raw

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3 <110> APPLICANT: HOWARD, JOHN A.
4   HOOD, ELIZABETH
5   JILKA, JOSEPH
7 <120> TITLE OF INVENTION: COMMERCIAL PRODUCTION OF LACCASE IN PLANTS
9 <130> FILE REFERENCE: 10015
11 <140> CURRENT APPLICATION NUMBER: 09/786,960
12 <141> CURRENT FILING DATE: 2001-03-12
14 <150> PRIOR APPLICATION NUMBER: 60/103,301
15 <151> PRIOR FILING DATE: 1998-10-05
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1500
23 <212> TYPE: DNA
24 <213> ORGANISM: Trametes versicolor
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1497)
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33   1           5           10           15
35 ccc gac ggc ttc ctt cgg gat gcc atc gtg gtc aac ggc gtg gtc cct      96
36 Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro
37   20           25           30
39 tcc ccg ctc atc acc ggg aag aag gga gac cgc ttc cag ctc aac gtc      144
40 Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val
41   35           40           45
43 gtc gac acc ttg acc aac cac agc atg ctc aag tcc act agt atc cac      192
44 Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His
45   50           55           60
47 tgg cac ggc ttc ttc cag gca ggc acc aac tgg gca gac gga ccc gcg      240
48 Trp His Gly Phe Phe Gln Ala Gly Thr Asn Trp Ala Asp Gly Pro Ala
49   65           70           75           80
51 ttc gtc aac cag tgc cct att gct tcc ggg cat tca ttt ctg tac gac      288
52 Phe Val Asn Gln Cys Pro Ile Ala Ser Gly His Ser Phe Leu Tyr Asp
53   85           90           95
55 ttc cat gtg ccc gac cag gca gga acg ttc tgg tac cac agt cat ctg      336
56 Phe His Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
57   100          105          110
59 tct acg caa tac tgt gac ggg ctg cga gga ccg ttc gtc gtg tac gac      384
60 Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
61   115          120          125
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63 ccc aag gat ccg cac gcc agc cgc tac gat gtt gac aac gag agc acg 432
64 Pro Lys Asp Pro His Ala Ser Arg Tyr Asp Val Asp Asn Glu Ser Thr
65 130 135 140
67 gtc atc acg ttg acc gac tgg tac cac acc gct gcc cgg ctc ggt ccc 480
68 Val Ile Thr Leu Thr Asp Trp Tyr His Thr Ala Ala Arg Leu Gly Pro
69 145 150 155 160
71 agg ttc cca ctc ggc gcg gac gcc acg ctc atc aat ggt ctt ggg cgg 528
72 Arg Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Leu Gly Arg
73 165 170 175
75 tcg gcc tcc act ccc acc gcc gcg ctt gct gtg atc aac gtc cag cac 576
76 Ser Ala Ser Thr Pro Thr Ala Ala Leu Ala Val Ile Asn Val Gln His
77 180 185 190
79 gga aag cgc tac cgc ttc cgt ctc gtt tcg atc tcg tgc gac ccg aac 624
80 Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Ile Ser Cys Asp Pro Asn
81 195 200 205
83 tac acg ttc agc atc gac ggg cac aat ctg acc gtc atc gag gtc gac 672
84 Tyr Thr Phe Ser Ile Asp Gly His Asn Leu Thr Val Ile Glu Val Asp
85 210 215 220
87 ggt atc aac agc cag cct ctc ctt gtc gac tct atc cag atc ttc gcc 720
88 Gly Ile Asn Ser Gln Pro Leu Leu Val Asp Ser Ile Gln Ile Phe Ala
89 225 230 235 240
91 gcg cag cgc tac tcc ttt gtg ttg aat gcg aac caa acg gtc ggc aac 768
92 Ala Gln Arg Tyr Ser Phe Val Leu Asn Ala Asn Gln Thr Val Gly Asn
93 245 250 255
95 tac tgg gtc cgc gcg aac ccg aac ttc gga acg gtt ggg ttc gcc ggg 816
96 Tyr Trp Val Arg Ala Asn Pro Asn Phe Gly Thr Val Gly Phe Ala Gly
97 260 265 270
99 ggg atc aac tcc gcc atc ctg cgc tac caa ggc gca cca gtc gcc gag 864
100 Gly Ile Asn Ser Ala Ile Leu Arg Tyr Gln Gly Ala Pro Val Ala Glu
101 275 280 285
103 ccc act acg acc cag acg acg tcg gtg atc ccg ctt atc gag acg aac 912
104 Pro Thr Thr Thr Gln Thr Thr Ser Val Ile Pro Leu Ile Glu Thr Asn
105 290 295 300
107 ttg cac ccc ctc gct cgc atg cct gtg cct ggc agc ccg aca ccc ggg 960
108 Leu His Pro Leu Ala Arg Met Pro Val Pro Gly Ser Pro Thr Pro Gly
109 305 310 315 320
111 ggc gtc gac aag gcg ctc aac ctc gcg ttt aac ttc aac ggc acc aac 1008
112 Gly Val Asp Lys Ala Leu Asn Leu Ala Phe Asn Phe Asn Gly Thr Asn
113 325 330 335
115 ttc ttc atc aac aac gcg act ttc acg ccg ccg acc gtc ccg gta ctc 1056
116 Phe Phe Ile Asn Asn Ala Thr Phe Thr Pro Pro Thr Val Pro Val Leu
117 340 345 350
119 ctc cag att ctg agc ggt gcg cag acc gca caa gac ctg ctc cct gca 1104
120 Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala
121 355 360 365
123 ggc tct gtc tac ccg ctc ccg gcc cac tcc acc atc gag atc acg ctg 1152
124 Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu
125 370 375 380
127 ccc gcg acc gcc ttg gcc ccg ggt gca ccg cac ccc ttc cac ctg cac 1200

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128 Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His
129 385                      390                      395 .                      400
131 ggt cac gcc ttc gcg gtc gtt cgc agc gcg ggg agc acc acg tat aac 1248
132 Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn
133                      405                      410                      415
135 tac aac gac ccg atc ttc cgc gac gtc gtg agc acg ggc acg ccc gcc 1296
136 Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
137                      420                      425                      430
139 gcg ggc gac aac gtc acg atc cgc ttc cag acg gac aac ccc ggg ccg 1344
140 Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro
141                      435                      440                      445
143 tgg ttc ctc cac tgc cac atc gac ttc cac ctc gac gcg ggc ttc gcg 1392
144 Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala
145                      450                      455                      460
147 atc gtg ttc gca gag gac gtt gcg gac gtg aag gcg gcg aac ccg gtt 1440
148 Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val
149 465                      470                      475                      480
151 ccg aag gcg tgg tgc gac ctg tgc ccg atc tac gac ggg ctg agc gag 1488
152 Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu
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159 <210> SEQ ID NO: 2
160 <211> LENGTH: 499
161 <212> TYPE: PRT
162 <213> ORGANISM: Trametes versicolor
164 <400> SEQUENCE: 2
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168 Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro
169 20 25 30
171 Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val
172 35 40 45
174 Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His
175 50 55 60
177 Trp His Gly Phe Phe Gln Ala Gly Thr Asn Trp Ala Asp Gly Pro Ala
178 65 70 75 80
180 Phe Val Asn Gln Cys Pro Ile Ala Ser Gly His Ser Phe Leu Tyr Asp
181 85 90 95
183 Phe His Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
184 100 105 110
186 Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
187 115 120 125
189 Pro Lys Asp Pro His Ala Ser Arg Tyr Asp Val Asp Asn Glu Ser Thr
190 130 135 140
192 Val Ile Thr Leu Thr Asp Trp Tyr His Thr Ala Ala Arg Leu Gly Pro
193 145 150 155 160
195 Arg Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Leu Gly Arg
196 165 170 175

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198 Ser Ala Ser Thr Pro Thr Ala Ala Leu Ala Val Ile Asn Val Gln His
199          180          185          190
201 Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Ile Ser Cys Asp Pro Asn
202          195          200          205
204 Tyr Thr Phe Ser Ile Asp Gly His Asn Leu Thr Val Ile Glu Val Asp
205          210          215          220
207 Gly Ile Asn Ser Gln Pro Leu Leu Val Asp Ser Ile Gln Ile Phe Ala
208 225          230          235          240
210 Ala Gln Arg Tyr Ser Phe Val Leu Asn Ala Asn Gln Thr Val Gly Asn
211          245          250          255
213 Tyr Trp Val Arg Ala Asn Pro Asn Phe Gly Thr Val Gly Phe Ala Gly
214          260          265          270
216 Gly Ile Asn Ser Ala Ile Leu Arg Tyr Gln Gly Ala Pro Val Ala Glu
217          275          280          285
219 Pro Thr Thr Thr Gln Thr Thr Ser Val Ile Pro Leu Ile Glu Thr Asn
220          290          295          300
222 Leu His Pro Leu Ala Arg Met Pro Val Pro Gly Ser Pro Thr Pro Gly
223 305          310          315          320
225 Gly Val Asp Lys Ala Leu Asn Leu Ala Phe Asn Phe Asn Gly Thr Asn
226          325          330          335
228 Phe Phe Ile Asn Asn Ala Thr Phe Thr Pro Pro Thr Val Pro Val Leu
229          340          345          350
231 Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala
232          355          360          365
234 Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu
235          370          375          380
237 Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His
238 385          390          395          400
240 Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn
241          405          410          415
243 Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
244          420          425          430
246 Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro
247          435          440          445
249 Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala
250          450          455          460
252 Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val
253 465          470          475          480
255 Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu
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265 <213> ORGANISM: Zea mays
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Globulin-1 promoter
270 <400> SEQUENCE: 3
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273 ccaaccaaac tttttgtggt atgttcctac actatgtaga tctacatgta ccattttggc 120
275 acaattacat atttacaaaa atgtttttcta taaatattag atttagttcg tttatttgaa 180
277 tttcttcgga aaattcacat ttaaactgca agtcactcga aacatggaaa accgtgcatg 240
279 caaaataaat gatatgcatg ttatctagca caagttacga ccgatttcag aagcagacca 300
281 gaatcttcaa gcaccatgct cactaaacat gaccgtgaac ttgttatcta gttgttttaa 360
283 aattgtataa aacacaaaata aagtcagaaa ttaatgaaac ttgtccacat gtcatgatat 420
285 catatataga ggttgatgata aaaatttgat aatgtttcgg taaagttgtg acgtactatg 480
287 ttagaaaacc taagtgcctt acacataaaa tcatagagtt tcaatgtagt tcaactcgaca 540
289 aagactttgt caagtgtccg ataaaaagta ctgcacaaag aagccgttgt cgatgtactg 600
291 ttcgtcgaga tctctttgtc gagtgtcaca ctaggcaaag tctttacgga gtgtttttca 660
293 ggctttgaca ctccgcaaag cgctcgattc cagtagtgac agtaatttgc atcaaaaata 720
295 gctgagagat ttaggccccg tttcaatctc acgggataaa gtttagcttc ctgctaaact 780
297 ttagctatat gaattgaagt gctaaagttt agtttcaatt accaccatta gctctcctgt 840
299 ttagattaca aatggctaaa agtagctaaa aaatagctgc taaagtttat ctgcgcgagat 900
301 tgaaacaggg ccttaaaatg agtcaactaa tagaccaact aattattagc tattagtcgt 960
303 tagcttcttt aatctaagct aaaaccaact aatagcttat ttgttgaatt acaattagct 1020
305 caacggaatt ctctgttttt ctaaaaaaa actgccccctc tcttacagca aattgtccgc 1080
307 tgcccgtcgt ccagatacaa tgaacgtacc tagtaggaac tcttttacac gctcggtcgc 1140
309 tcgcccgcga tcggagtccc cggaacacga caccactgtg gaacacgaca aagtctgctc 1200
311 agaggcgcc acaccctggc gtgcaccgag ccggagcccc gataagcacg gtaaggagag 1260
313 tacggcgga cgtggcgacc cgtgtgtctg ctgccacgca gccttcctcc acgtagccgc 1320
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317 ttctgcatac agccaaccca a 1401
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/786,960

DATE: 08/01/2002

TIME: 11:13:51

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